Raw Sequence Listing Error Summary

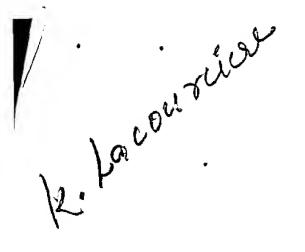
Hq Bill

SERIAL NUMBER: 09

ERROR DETECTED SUGGESTED CORRECTION

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping". Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping". The rules require that a line not exceed 72 characters in length. This includes spaces. Incorrect Line Length Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers. Numbering This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Non-ASCII Please ensure your subsequent submission is saved in ASCII text so that it can be processed. Variable Length Sequence(s) ____ contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing. A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid Patentin ver. 2.0 "bug" sequence(s) ______. Normally, Patentln would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences. **Skipped Sequences** Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence: (OLD RULES) (2) INFORMATION FOR SEQ ID NO:X: (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS") (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: This sequence is intentionally skipped Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s). **Skipped Sequences** Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence. (NEW RULES) <210> sequence id number <400> sequence id number 000 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing. (NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents. 11 _____ Use of <213>Organism Sequence(s) _____ are missing this mandatory field or its response. (NEW RULES) Use of <220>Feature are missing the <220>Feature and associated headings. Sequence(s) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown" (NEW RULES) Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules) Please do not use "Copy to Disk" function of Patentln version 2.0. This causes a corrupted 13 _____ PatentIn ver. 2.0 "bug" file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).

Instead, please use "File Manager" or any other means to copy file to floppy disk.



RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/383,894A

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Output Set: N:\CRF3\03302001\1383894A.raw

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Does Not Comply Corrected Diskette Needed

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RAW SEQUENCE LISTING
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RAW SEQUENCE LISTING
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DATE: 03/30/2001
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288	705					710			Arg		715					720
291					725				Phe	730					735	
294				740					Tyr 745					750		
297			755					760	Met				765			
300		770					775		Glu			780				
303	785					790			Leu		795			_	_	800
306					805				Asn	810					815	
200	val	тте	ser	val	ттр	GIU	тте	val	Gly	GIN	GIn	GTA	GLY	GTA	Leu	Ser

<210>	6
<211>	17
<212>	DNA .
<213>	Artificial Sequence
<220>	
<223>	Description of Artificial Sequence: Primer Sequence
<400>	6 atgga gmgnecy) see Jen 10 m
tingcha	atgga gmgncy
	Sun Surmary

VERIFICATION SUMMARY

DATE: 03/30/2001 PATENT APPLICATION: US/09/383,894A TIME: 15:37:28

Input Set : A:\00400191.app

Output Set: N:\CRF3\03302001\I383894A.raw

L:1216 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6 L:1216 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6

L:1216 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6